SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> DNA Encoding Sucrose PTS Enzyme II

<130> B644MSOP1027

<150> JP 11-189512
<151> 1999-07-02

<160> 21

<170> PatentIn Ver. 2.0

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3

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atg gac cat aag gac ctc gcg caa cgc atc ctg cgc gac att ggc ggc   3826
Met Asp His Lys Asp Leu Ala Gln Arg Ile Leu Arg Asp Ile Gly Gly
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gaa gac aac att gtc gcc gcc gca cac tgt gca acg cgt tta cgc ctc   3874
Glu Asp Asn Ile Val Ala Ala Ala His Cys Ala Thr Arg Leu Arg Leu
            20                  25                  30

gtg ctc aaa gac acc aag gat gtg gat cgc caa agt ctg gat gat gat   3922
Val Leu Lys Asp Thr Lys Asp Val Asp Arg Gln Ser Leu Asp Asp Asp
            35                  40                  45

cca gat ctg aaa ggc acc ttt gaa act ggc ggc atg ttc cag atc atc   3970
Pro Asp Leu Lys Gly Thr Phe Glu Thr Gly Gly Met Phe Gln Ile Ile
         50                  55                  60

gtc ggg cca ggc gat gtg gat cat gtt ttc aaa gaa ctc gat gac gca   4018
Val Gly Pro Gly Asp Val Asp His Val Phe Lys Glu Leu Asp Asp Ala
 65               70                  75                  80

acc tcc aaa gac atc gct gtg tcc aca gag cag ctc aaa gat gtt gtg   4066
Thr Ser Lys Asp Ile Ala Val Ser Thr Glu Gln Leu Lys Asp Val Val
                 85                  90                  95

gct aac aac gcc aac tgg ttc agc cgt gct gtg aag gta ttg gcg gac   4114
Ala Asn Asn Ala Asn Trp Phe Ser Arg Ala Val Lys Val Leu Ala Asp
                100                 105                 110

att ttc gtc ccg ctg att cca atc ttg gtt ggt ggc ggt ctg ctc atg   4162
Ile Phe Val Pro Leu Ile Pro Ile Leu Val Gly Gly Gly Leu Leu Met
                115                 120                 125

gct atc aac aat gtg ttg gtt gcg cag gat ctg ttc ggt ccg caa tca   4210
Ala Ile Asn Asn Val Leu Val Ala Gln Asp Leu Phe Gly Pro Gln Ser
            130                 135                 140

ctg gtg gag atg ttc cct cag atc agc ggt gtt gct gag atg atc aac   4258
Leu Val Glu Met Phe Pro Gln Ile Ser Gly Val Ala Glu Met Ile Asn
145                 150                 155                 160

ctg atg gca tct gcg ccg ttc gcg ttc ttg cca gtg ttg gtt ggt ttc   4306
Leu Met Ala Ser Ala Pro Phe Ala Phe Leu Pro Val Leu Val Gly Phe
                165                 170                 175
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4

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acc gca acc aag cgt ttc ggt ggc aat gag ttc ctg ggc gcc ggc att    4354
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ggt atg gcg atg gtg ttc cca acc ctg gtt aac ggc tac gac gtg gcc    4402
Gly Met Ala Met Val Phe Pro Thr Leu Val Asn Gly Tyr Asp Val Ala
        195             200             205

gcc acc atg acc gcg ggc gaa atg cca atg tgg tcc ctg ttt ggt ttg    4450
Ala Thr Met Thr Ala Gly Glu Met Pro Met Trp Ser Leu Phe Gly Leu
        210             215             220

gat gtt gct caa gct ggt tac cag ggc acc gtg ctt cct gtg ctg gtg    4498
Asp Val Ala Gln Ala Gly Tyr Gln Gly Thr Val Leu Pro Val Leu Val
225             230             235             240

gtc tct tgg att ctg gca acg atc gag aag ttc ctg cac aag cga ctc    4546
Val Ser Trp Ile Leu Ala Thr Ile Glu Lys Phe Leu His Lys Arg Leu
        245             250             255

atg ggc act gca gac ttc ctg atc acc cca gtg ttg act ctg ctg ctc    4594
Met Gly Thr Ala Asp Phe Leu Ile Thr Pro Val Leu Thr Leu Leu Leu
         260             265             270

acc ggc ttc ctt acg ttc att gct att ggt cca gca atg cgc tgg gtg    4642
Thr Gly Phe Leu Thr Phe Ile Ala Ile Gly Pro Ala Met Arg Trp Val
        275             280             285

ggt gac ttg ctg gca cac ggt ctg cag gga ctc tat gat ttc ggt ggt    4690
Gly Asp Leu Leu Ala His Gly Leu Gln Gly Leu Tyr Asp Phe Gly Gly
        290             295             300

cca gtc ggc ggt ctg ctt ttc ggt ctg gtc tac tca cca atc gtt atc    4738
Pro Val Gly Gly Leu Leu Phe Gly Leu Val Tyr Ser Pro Ile Val Ile
305             310             315             320

act ggt ctg cac cag tcc ttc ccg cca att gag ctg gag ctg ttc aac    4786
Thr Gly Leu His Gln Ser Phe Pro Pro Ile Glu Leu Glu Leu Phe Asn
        325             330             335

cag ggt gga tcc ttc atc ttc gca acc gca tcc atg gcc aat atc gcg    4834
Gln Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser Met Ala Asn Ile Ala
        340             345             350

cag ggt gca gca tgt ttg gca gtg ttc ttc cta gcg aag agt gaa aag    4882
Gln Gly Ala Ala Cys Leu Ala Val Phe Phe Leu Ala Lys Ser Glu Lys
        355             360             365

ctc aag ggc ctt gca ggt gct tca ggt gtc tcc gct gtt ctt ggt att    4930
Leu Lys Gly Leu Ala Gly Ala Ser Gly Val Ser Ala Val Leu Gly Ile
        370             375             380

aca gag cct gcg atc ttc ggt gtg aac ctt cgc ctg cgc tgg ccg ttc    4978
Thr Glu Pro Ala Ile Phe Gly Val Asn Leu Arg Leu Arg Trp Pro Phe
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5

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Tyr Ile Gly Ile Gly Thr Ala Ala Ile Gly Gly Ala Leu Ile Ala Leu
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ttt gat atc aag gca gtt gcg ttg ggc gct gca ggt ttc ttg ggt gtt    5074
Phe Asp Ile Lys Ala Val Ala Leu Gly Ala Ala Gly Phe Leu Gly Val
                    420                    425                    430
gtt tct att gat gct cca gat atg gtc atg ttc ttg gtt tgc gcg gta    5122
Val Ser Ile Asp Ala Pro Asp Met Val Met Phe Leu Val Cys Ala Val
                    435                    440                    445
gtt acc ttt gtc atc gca ttc ggc gca gcg att gct tat ggc ctt tac    5170
Val Thr Phe Val Ile Ala Phe Gly Ala Ala Ile Ala Tyr Gly Leu Tyr
                    450                    455                    460
ttg gtt cgc cgc aac ggc agc att gat cca gat gca acc gct gct cca    5218
Leu Val Arg Arg Asn Gly Ser Ile Asp Pro Asp Ala Thr Ala Ala Pro
465                    470                    475                    480
gtg cct gca gga acg acc aaa gcc gaa gca gaa gca ccc gca gaa ttt    5266
Val Pro Ala Gly Thr Thr Lys Ala Glu Ala Glu Ala Pro Ala Glu Phe
                    485                    490                    495
tca aac gat tcc acc atc atc cag gca cct ttg acc ggt gaa gct atc    5314
Ser Asn Asp Ser Thr Ile Ile Gln Ala Pro Leu Thr Gly Glu Ala Ile
                    500                    505                    510
gca ctg agc agc gtc agc gat gcc atg ttt gcc agc gga aag ctt ggc    5362
Ala Leu Ser Ser Val Ser Asp Ala Met Phe Ala Ser Gly Lys Leu Gly
                    515                    520                    525
tca ggt gtt gcg atc gtc ccc acc aag ggg cag ctg gtt tca cca gtg    5410
Ser Gly Val Ala Ile Val Pro Thr Lys Gly Gln Leu Val Ser Pro Val
                    530                    535                    540
agc gga aag atc gtg gtg gcc ttc cca tct ggt cac gct ttc gca gtc    5458
Ser Gly Lys Ile Val Val Ala Phe Pro Ser Gly His Ala Phe Ala Val
545                    550                    555                    560
cgc act aag gct gag gat ggt tcc aat gtg gat atc ttg atg cac att    5506
Arg Thr Lys Ala Glu Asp Gly Ser Asn Val Asp Ile Leu Met His Ile
                    565                    570                    575
ggt ttc gac acc gta aac ctc aac ggc acg cac ttt aac ccg ctg aag    5554
Gly Phe Asp Thr Val Asn Leu Asn Gly Thr His Phe Asn Pro Leu Lys
                    580                    585                    590
aag cag ggc gat gaa gtc aaa gca ggg gag ctg ctg tgt gaa ttc gat    5602
Lys Gln Gly Asp Glu Val Lys Ala Gly Glu Leu Leu Cys Glu Phe Asp
                    595                    600                    605
att gat gcc att aag gct gca ggt tat gag gta acc acg ccg att gtt    5650
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Ile Asp Ala Ile Lys Ala Ala Gly Tyr Glu Val Thr Thr Pro Ile Val
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gtt tcg aat tac aag aaa acc gga cct gta aac act tac ggt ttg ggc   5698
Val Ser Asn Tyr Lys Lys Thr Gly Pro Val Asn Thr Tyr Gly Leu Gly
625   630   635   640

gaa att gaa gcg gga gcc aac ctg ctc aac gtc gca aag aaa gaa gcg   5746
Glu Ile Glu Ala Gly Ala Asn Leu Leu Asn Val Ala Lys Lys Glu Ala
             645   650   655

gtg cca gca aca cca taagttgaaa ccttgagtgt tcgcacacag gttagactag   5801
Val Pro Ala Thr Pro
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gggacgtgac tctacgcatc tttgacaccg gtacccgtac gcttcgagat tttaaacctg 5861
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<210> 2
<211> 661
<212> PRT
<213> Brevibacterium lactofermentum

<400> 2
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Glu Asp Asn Ile Val Ala Ala Ala His Cys Ala Thr Arg Leu Arg Leu
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Val Leu Lys Asp Thr Lys Asp Val Asp Arg Gln Ser Leu Asp Asp Asp
         35   40   45
Pro Asp Leu Lys Gly Thr Phe Glu Thr Gly Gly Met Phe Gln Ile Ile
     50   55   60
Val Gly Pro Gly Asp Val Asp His Val Phe Lys Glu Leu Asp Asp Ala
65   70   75   80
Thr Ser Lys Asp Ile Ala Val Ser Thr Glu Gln Leu Lys Asp Val Val
         85   90   95
Ala Asn Asn Ala Asn Trp Phe Ser Arg Ala Val Lys Val Leu Ala Asp
         100   105   110
Ile Phe Val Pro Leu Ile Pro Ile Leu Val Gly Gly Gly Leu Leu Met
        115   120   125
Ala Ile Asn Asn Val Leu Val Ala Gln Asp Leu Phe Gly Pro Gln Ser
        130   135   140
Leu Val Glu Met Phe Pro Gln Ile Ser Gly Val Ala Glu Met Ile Asn
145   150   155   160

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Leu Met Ala Ser Ala Pro Phe Ala Phe Leu Pro Val Leu Val Gly Phe
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Thr Ala Thr Lys Arg Phe Gly Gly Asn Glu Phe Leu Gly Ala Gly Ile
            180             185             190
Gly Met Ala Met Val Phe Pro Thr Leu Val Asn Gly Tyr Asp Val Ala
            195             200             205
Ala Thr Met Thr Ala Gly Glu Met Pro Met Trp Ser Leu Phe Gly Leu
    210             215             220
Asp Val Ala Gln Ala Gly Tyr Gln Gly Thr Val Leu Pro Val Leu Val
225             230             235             240
Val Ser Trp Ile Leu Ala Thr Ile Glu Lys Phe Leu His Lys Arg Leu
            245             250             255
Met Gly Thr Ala Asp Phe Leu Ile Thr Pro Val Leu Thr Leu Leu Leu
            260             265             270
Thr Gly Phe Leu Thr Phe Ile Ala Ile Gly Pro Ala Met Arg Trp Val
            275             280             285
Gly Asp Leu Leu Ala His Gly Leu Gln Gly Leu Tyr Asp Phe Gly Gly
    290             295             300
Pro Val Gly Gly Leu Leu Phe Gly Leu Val Tyr Ser Pro Ile Val Ile
305             310             315             320
Thr Gly Leu His Gln Ser Phe Pro Pro Ile Glu Leu Glu Leu Phe Asn
            325             330             335
Gln Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser Met Ala Asn Ile Ala
            340             345             350
Gln Gly Ala Ala Cys Leu Ala Val Phe Phe Leu Ala Lys Ser Glu Lys
    355             360             365
Leu Lys Gly Leu Ala Gly Ala Ser Gly Val Ser Ala Val Leu Gly Ile
    370             375             380
Thr Glu Pro Ala Ile Phe Gly Val Asn Leu Arg Leu Arg Trp Pro Phe
385             390             395             400
Tyr Ile Gly Ile Gly Thr Ala Ala Ile Gly Gly Ala Leu Ile Ala Leu
            405             410             415
Phe Asp Ile Lys Ala Val Ala Leu Gly Ala Ala Gly Phe Leu Gly Val
            420             425             430
Val Ser Ile Asp Ala Pro Asp Met Val Met Phe Leu Val Cys Ala Val
            435             440             445
Val Thr Phe Val Ile Ala Phe Gly Ala Ala Ile Ala Tyr Gly Leu Tyr
    450             455             460
Leu Val Arg Arg Asn Gly Ser Ile Asp Pro Asp Ala Thr Ala Ala Pro
465             470             475             480
Val Pro Ala Gly Thr Thr Lys Ala Glu Ala Glu Ala Pro Ala Glu Phe
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Ala Leu Ser Ser Val Ser Asp Ala Met Phe Ala Ser Gly Lys Leu Gly
                 515                    520                    525
Ser Gly Val Ala Ile Val Pro Thr Lys Gly Gln Leu Val Ser Pro Val
             530                    535                    540
Ser Gly Lys Ile Val Val Ala Phe Pro Ser Gly His Ala Phe Ala Val
545                    550                    555                    560
Arg Thr Lys Ala Glu Asp Gly Ser Asn Val Asp Ile Leu Met His Ile
                 565                    570                    575
Gly Phe Asp Thr Val Asn Leu Asn Gly Thr His Phe Asn Pro Leu Lys
             580                    585                    590
Lys Gln Gly Asp Glu Val Lys Ala Gly Glu Leu Leu Cys Glu Phe Asp
                 595                    600                    605
Ile Asp Ala Ile Lys Ala Ala Gly Tyr Glu Val Thr Thr Pro Ile Val
             610                    615                    620
Val Ser Asn Tyr Lys Lys Thr Gly Pro Val Asn Thr Tyr Gly Leu Gly
625                    630                    635                    640
Glu Ile Glu Ala Gly Ala Asn Leu Leu Asn Val Ala Lys Lys Glu Ala
                 645                    650                    655
Val Pro Ala Thr Pro
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<210> 3
<211> 44
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Sau3AI cassette

<220>
<221> misc_feature
<222> (44)
<223> complementary strand extends a single strand having
      a sequence of 3'-ctag-5' at this position in the
      direction of 5' from 3'

<400> 3
gtacatattg tcgttagaac gcgtaatacg actcactata ggga   44

<210> 4
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: EcoRI cassette

<220>
<221> misc_feature
<222> (47)
<223> complementary strand extends a single strand having
      a sequence of 3'-ttaa-5' at this position in the
      direction of 5' from 3'

<400> 4
gtacatattg tcgttagaac gcgtaatacg actcactata gggagag   47

<210> 5
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HindIII cassette

<220>
<221> misc_feature
<222> (46)
<223> complementary strand extends a single strand having
      a sequence of 3'-tcga-5' at this position in the
      direction of 5' from 3'

<400> 5
gtacatattg tcgttagaac gcgtaatacg actcactata gggaga   46

<210> 6
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
<222> (48)..(51)
<223> complementary strand does not exist

<400> 6
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<210> 7
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SalI cassette

<220>
<221> misc_feature
<222> (47)
<223> complementary strand extends a single strand having
      a sequence of 3'-agct-5' at this position in the
      direction of 5' from 3'

<400> 7
gtacatattg tcgttagaac gcgtaatacg actcactata gggagag   47

<210> 8
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: XbaI cassette

<220>
<221> misc_feature
<222> (47)
<223> complementary strand extends a single strand having

a sequence of 3'-gatc-5' at this position in the
direction of 5' from 3'

<400> 8
gtacatattg tcgttagaac gcgtaatacg actcactata gggagat   47

<210> 9
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 9
cgtcttgcga ggattcagcg agctg   25

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 10
agctggattt cggccatgaa ttcta   25

<210> 11
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 11
gatctgttcg gtccgcaatc act   23

<210> 12
<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 12
cactggtgga gatgttccct cagat   25

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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<400> 13
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<210> 14
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR
<400> 14
cgcgcagggt gcagcatgtt tggc   24

<210> 15
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 15
gggccttgca ggtgcttcag gtgtc   25

<210> 16
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 16
ccgctgttct tggtattaca gagcc   25

<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 17
gcagcgtcag cgatgccatg tttgc   25

<210> 18
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 18
gcttggctca ggtgttgcga tcgtc   25

<210> 19
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: cassette
      primer l

<400> 19
gtacatattg tcgttagaac gcggtaatac gactca   36

<210> 20
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: cassette
      primer 2

<400> 20
cgttagaacg cgtaatacga ctcactatag ggaga   35

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 21
cgctactgct gaacgaacat gtcc   24